# RAW SEQUENCE LISTING

**The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) no errors detected.**

Application Serial Number: _____ *10/768, 886 B*

Source: _____ *1 FW/6*

Date Processed by STIC: _____ *06/21/2006*

# *ENTERED*

RAW SEQUENCE LISTING                    DATE: 06/21/2006
PATENT APPLICATION:  US/10/768,886B     TIME: 15:18:17

Input Set : A:\MAPK5 (Supp).txt
Output Set: N:\CRF4\06212006\J768886B.raw

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 3 <110> APPLICANT: Board of Trustees for University of Arkansas
 5 <120> TITLE OF INVENTION: Mitogen-Activated Protein Kinase and Method of Use to
Enhance
 6        Biotic and Abiotic Stress Tolerance in Plants
 8 <130> FILE REFERENCE: UAF-03-14
C--> 10 <140> CURRENT APPLICATION NUMBER: US/10/768,886B
11 <141> CURRENT FILING DATE: 2004-01-31
13 <160> NUMBER OF SEQ ID NOS: 10
15 <170> SOFTWARE: PatentIn version 3.2
17 <210> SEQ ID NO: 1
18 <211> LENGTH: 1396
19 <212> TYPE: DNA
20 <213> ORGANISM: Oryza sativa
22 <400> SEQUENCE: 1
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25 aggaggaggg attagggatg gacggggcgc cggtggcgga gttcaggccg acgatgacgc     120
27 acggcggccg gtacctgctc tacgacatct tcgggaacaa gttcgaggtg acgaacaagt     180
29 accagccgcc catcatgccc attggccgcg gcgcctacgg gatcgtctgc tccgtgatga     240
31 actttgagac gagggagatg gtggcgataa agaagatcgc caacgcgttc aacaacgaca     300
33 tggacgccaa gcgcacgctc cgggagatca agctcctcag gcacctcgac cacgagaaca     360
35 tcataggcat cagggatgtg atcccgccgc cgatccctca ggcgttcaac gacgtctaca     420
37 tcgccacgga gctcatggac accgacctcc atcacatcat ccgctccaac caagaactgt     480
39 cagaagagca ctgccagtat ttcctgtacc agatcctgcg ggggctcaag tacatccact     540
41 cggcgaacgt gatccaccgc gacctgaagc cgagcaacct gctgctgaac gccaactgcg     600
43 acctcaagat ctgcgacttc gggctggcgc ggccgtcgtc ggagagcgac atgatgacgg     660
45 agtacgtggt caccccggtgg taccgcgcgc cggagctgct gctcaactcc accgactact     720
47 ccgccgccat cgacgtctgg tccgtcggct gcatcttcat ggagctcatc aaccgccagc     780
49 cgctcttccc cggcagggac cacatgcacc agatgcgcct catcaccgag gtgatcggga     840
51 cgccgacgga cgacgagctg gggttcatac ggaacgagga cgcgaggaag tacatgaggc     900
53 acctgccgca gtacccgcgc cggacgttcg cgagcatgtt cccgcgggtg cagcccgccg     960
55 cgctcgacct catcgagagg atgctcacct tcaacccgct gcagagaatc acagttgagg    1020
57 aggcgctcga tcatccttac ctagagagat tgcacgacat cgccgatgag cccatctgcc    1080
59 tggagccctt ctccttcgac ttcgagcaga aggctctaaa cgaggaccaa atgaagcagc    1140
61 tgatcttcaa cgaagcgatc gagatgaacc caaacatccg gtactagatt gaatcaccat    1200
63 ggaaatgaga tcccgtctat acctgctttg tacatatgat caagattgag agccgggtag    1260
65 actgaacatt gcatttgttt gtttgttgat gttcgaaacc cacattctct gcaagttgtg    1320
67 gctgctttgt atgatatatg gtactatgtt cgaataaaag ggtttggaac tttggattaa    1380
69 aaaaaaaaaa aaaaaa                                                    1396
72 <210> SEQ ID NO: 2
73 <211> LENGTH: 368
74 <212> TYPE: PRT
75 <213> ORGANISM: Oryza sativa
77 <400> SEQUENCE: 2
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84          20                   25                   30
87 Asn Lys Tyr Gln Pro Pro Ile Met Pro Ile Gly Arg Gly Ala Tyr Gly
88          35                   40                   45
91 Ile Val Cys Ser Val Met Asn Phe Glu Thr Arg Glu Met Val Ala Ile
92     50                   55                   60
95 Lys Lys Ile Ala Asn Ala Phe Asn Asn Asp Met Asp Ala Lys Arg Thr
96 65                   70                   75                   80
99 Leu Arg Glu Ile Lys Leu Leu Arg His Leu Asp His Glu Asn Ile Ile
100                  85                   90                   95
103 Gly Ile Arg Asp Val Ile Pro Pro Ile Pro Gln Ala Phe Asn Asp
104              100                  105                  110
107 Val Tyr Ile Ala Thr Glu Leu Met Asp Thr Asp Leu His His Ile Ile
108              115                  120                  125
111 Arg Ser Asn Gln Glu Leu Ser Glu Glu His Cys Gln Tyr Phe Leu Tyr
112     130                  135                  140
115 Gln Ile Leu Arg Gly Leu Lys Tyr Ile His Ser Ala Asn Val Ile His
116 145                  150                  155                  160
119 Arg Asp Leu Lys Pro Ser Asn Leu Leu Leu Asn Ala Asn Cys Asp Leu
120                  165                  170                  175
123 Lys Ile Cys Asp Phe Gly Leu Ala Arg Pro Ser Ser Glu Ser Asp Met
124              180                  185                  190
127 Met Thr Glu Tyr Val Val Thr Arg Trp Tyr Arg Ala Pro Glu Leu Leu
128          195                  200                  205
131 Leu Asn Ser Thr Asp Tyr Ser Ala Ala Asp Val Trp Ser Val Gly Cys
132     210                  215                  220
135 Ile Phe Met Glu Leu Ile Asn Arg Gln Pro Leu Phe Pro Gly Arg Asp
136 225                  230                  235                  240
139 His Met His Gln Met Arg Leu Ile Thr Glu Val Ile Gly Thr Pro Thr
140              245                  250                  255
143 Asp Asp Glu Leu Gly Phe Ile Arg Asn Glu Asp Ala Arg Lys Tyr Met
144          260                  265                  270
147 Arg His Leu Pro Gln Tyr Pro Arg Arg Thr Phe Ala Ser Met Phe Pro
148          275                  280                  285
151 Arg Val Gln Pro Ala Ala Leu Asp Leu Ile Glu Arg Met Leu Thr Phe
152     290                  295                  300
155 Asn Pro Leu Gln Arg Ile Thr Val Glu Glu Ala Leu Asp His Pro Tyr
156 305                  310                  315                  320
159 Leu Glu Arg Leu His Asp Ile Ala Asp Glu Pro Ile Cys Leu Glu Pro
160                  325                  330                  335
163 Phe Ser Phe Asp Phe Glu Gln Lys Ala Leu Asn Glu Asp Gln Met Lys
164          340                  345                  350
167 Gln Leu Ile Phe Asn Glu Ala Ile Glu Met Asn Pro Asn Ile Arg Tyr
168          355                  360                  365
171 <210> SEQ ID NO: 3
172 <211> LENGTH: 1084
173 <212> TYPE: DNA
174 <213> ORGANISM: Oryza sativa
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RAW SEQUENCE LISTING          DATE: 06/21/2006
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Input Set : A:\MAPK5 (Supp).txt
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176 <400> SEQUENCE: 3
177 agagagtcag ataaggtcgt taattaggtt ggtcaattcg gctgcttgcg gcgagagaag     60
179 aggaggaggg attagggatg gacggggcgc cggtggcgga gttcaggccg acgatgacgc    120
181 acggcggccg gtacctgctc tacgacatct tcgggaacaa gttcgaggtg acgaacaagt    180
183 accagccgcc catcatgccc attggccgcg gcgcctacgg gatcgtctgc tccgtgatga    240
185 actttgagac gagggagatg gtggcgataa agaagatcgc caactgcgac ctcaagatct    300
187 gcgacttcgg gctggcgcgg ccgtcgtcgg agagcgacat gatgacggag tacgtggtca    360
189 cccggtggta ccgcgcgccg gagctgctgc tcaactccac cgactactcc gccgccatcg    420
191 acgtctggtc cgtcggctgc atcttcatgg agctcatcaa ccgccagccg ctcttccccg    480
193 gcagggacca catgcaccag atgcgcctca tcaccgaggt gatcgggacg ccgacggacg    540
195 acgagctggg gttcatacgg aacgaggacg cgaggaagta catgaggcac ctgccgcagt    600
197 acccgcgccg gacgttcgcg agcatgttcc cgcgggtgca gcccgccgcg ctcgacctca    660
199 tcgagaggat gctcaccttc aacccgctgc agagaatcac agttgaggag gcgctcgatc    720
201 atccttacct agagagattg cacgacatcg ccgatgagcc catctgcctg gagcccttct    780
203 ccttcgactt cgagcagaag gctctaaacg aggaccaaat gaagcagctg atcttcaacg    840
205 aagcgatcga gatgaaccca aacatccggt actagattga atcaccatgg aaatgagatc    900
207 ccgtctatac ctgctttgta catatgatca agattgagag ccgggtagac tgaacattgc    960
209 atttgtttgt tgttgatgt tcgaaaccca cattctctgc aagttgtggc tgctttgtat   1020
211 gatatatggt actatgttcg aataaaaggg tttggaactt tggattaaaa aaaaaaaaaa   1080
213 aaaa                                                               1084
216 <210> SEQ ID NO: 4
217 <211> LENGTH: 266
218 <212> TYPE: PRT
219 <213> ORGANISM: Oryza sativa
221 <400> SEQUENCE: 4
223 Met Met Asp Gly Ala Pro Val Ala Glu Phe Arg Pro Thr Met Thr His
224 1               5                   10                  15
227 Gly Gly Arg Tyr Leu Leu Tyr Asp Ile Phe Gly Asn Lys Phe Glu Val
228             20                  25                  30
231 Thr Asn Lys Tyr Gln Pro Pro Ile Met Pro Ile Gly Arg Gly Ala Tyr
232         35                  40                  45
235 Gly Ile Val Cys Ser Val Met Asn Phe Glu Thr Arg Glu Met Val Ala
236     50                  55                  60
239 Ile Lys Lys Ile Ala Asn Cys Asp Leu Lys Ile Cys Asp Phe Gly Leu
240 65                  70                  75                  80
243 Ala Arg Pro Ser Ser Glu Ser Asp Met Met Thr Glu Tyr Val Val Thr
244                 85                  90                  95
247 Arg Trp Tyr Arg Ala Pro Glu Leu Leu Leu Asn Ser Thr Asp Tyr Ser
248                 100                 105                 110
251 Ala Ala Ile Asp Val Trp Ser Val Gly Cys Ile Phe Met Glu Leu Ile
252             115                 120                 125
255 Asn Arg Gln Pro Leu Phe Pro Gly Arg Asp His Met His Gln Met Arg
256     130                 135                 140
259 Leu Ile Thr Glu Val Ile Gly Thr Pro Thr Asp Asp Glu Leu Gly Phe
260 145                 150                 155                 160
263 Ile Arg Asn Glu Asp Ala Arg Lys Tyr Met Arg His Leu Pro Gln Tyr
264                 165                 170                 175
267 Pro Arg Arg Thr Phe Ala Ser Met Phe Pro Arg Val Gln Pro Ala Ala
268             180                 185                 190
```

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271 Leu Asp Leu Ile Glu Arg Met Leu Thr Phe Asn Pro Leu Gln Arg Ile
272         195                 200                 205
275 Thr Val Glu Glu Ala Leu Asp His Pro Tyr Leu Glu Arg Leu His Asp
276         210                 215                 220
279 Ile Ala Asp Glu Pro Ile Cys Leu Glu Pro Phe Ser Phe Asp Phe Glu
280 225                 230                 235                 240
283 Gln Lys Ala Leu Asn Glu Asp Gln Met Lys Gln Leu Ile Phe Asn Glu
284                 245                 250                 255
287 Ala Ile Glu Met Asn Pro Asn Ile Arg Tyr
288                 260                 265
291 <210> SEQ ID NO: 5
292 <211> LENGTH: 26
293 <212> TYPE: DNA
294 <213> ORGANISM: Artificial
296 <220> FEATURE:
297 <223> OTHER INFORMATION: gene-specific primer containing restriction site
299 <400> SEQUENCE: 5
300 cgggatccgt cggctgcatc ttcatg                                    26
303 <210> SEQ ID NO: 6
304 <211> LENGTH: 25
305 <212> TYPE: DNA
306 <213> ORGANISM: Artificial
308 <220> FEATURE:
309 <223> OTHER INFORMATION: gene-specific primer containing restriction site
311 <400> SEQUENCE: 6
312 gctctagatt caatctagta ccgga                                     25
315 <210> SEQ ID NO: 7
316 <211> LENGTH: 20
317 <212> TYPE: DNA
318 <213> ORGANISM: Artificial
320 <220> FEATURE:
321 <223> OTHER INFORMATION: gene-specific primer containing restriction site
323 <400> SEQUENCE: 7
324 gagttcaggc cgacgatgac                                           20
327 <210> SEQ ID NO: 8
328 <211> LENGTH: 20
329 <212> TYPE: DNA
330 <213> ORGANISM: Artificial
332 <220> FEATURE:
333 <223> OTHER INFORMATION: gene-specific primer containing restriction site
335 <400> SEQUENCE: 8
336 atcggcgatg tcgtgcaatc                                           20
339 <210> SEQ ID NO: 9
340 <211> LENGTH: 368
341 <212> TYPE: PRT
342 <213> ORGANISM: Triticum aestivum
344 <400> SEQUENCE: 9
346 Met Asp Gly Ala Pro Val Ala Glu Phe Arg Pro Thr Met Thr His Gly
347 1                 5                 10                  15
```

```
350 Gly Arg Phe Leu Leu Tyr Asn Ile Phe Gly Asn Gln Phe Glu Thr Thr
351         20              25              30
354 Ala Lys Tyr Gln Pro Pro Ile Met Pro Ile Gly Lys Gly Ala Tyr Gly
355         35              40              45
358 Ile Val Cys Ser Val Met Asn Phe Glu Thr Arg Glu Met Val Ala Ser
359         50              55.             60
362 Lys Lys Ile Ala Asn Ala Phe Asp Asn Asn Met Asp Ala Lys Arg Thr
363 65              70              75              80
366 Leu Arg Glu Ile Lys Leu Leu Leu Arg His Leu Asp Glu Asn Ile Val
367             85              90              95
370 Gly Leu Arg Asp Val Ile Pro Pro Ala Ile Pro Gln Ser Glu Asn Asp
371             100             105             110
374 Val Tyr Ile Ala Thr Glu Leu Met Asp Thr Asp Leu His His Ile Ile
375         115             120             125
378 Arg Ser Asn Gly Glu Leu Ser Glu Glu His Glu Gln Tyr Phe Leu Tyr
379     130             135             140
382 Gln Leu Leu Arg Gly Leu Lys Tyr Ile His Ser Ala Asn Val Ile His
383 145             150             155             160
386 Arg Asp Leu Lys Pro Ser Asn Leu Leu Leu Asn Ala Asn Cys Asp Leu
387             165             170             175
390 Lys Ile Cys Asp Phe Gly Leu Ala Arg Pro Ser Ser Glu Ser Asp Met
391             180             185             190
394 Met Thr Glu Tyr Val Val Thr Arg Trp Tyr Arg Ala Pro Glu Leu Leu
395         195             200             205'
398 Leu Asn Ser Thr Asp Tyr Ser Ala Asn Ile Asp Val Trp Ser Val Gly
399     210             215             220
402 Cys Ile Phe Met Glu Leu Ile Asn Arg Ala Pro Leu Phe Pro Gly Arg
403 225             230             235             240
406 Asp His Met His Gln Met Arg Leu Ile Thr Glu Val Ile Gly Thr Pro
407             245             250             255
410 Thr Asp Asp Asp Leu Gly Phe Ile Arg Asn Glu Asp Ala Arg Arg Tyr
411             260             265             270
414 Met Arg His Leu Pro Gln Phe Pro Arg Arg Ser Phe Pro Gly Phe Pro
415         275             280             285
418 Lys Val Gln Pro Ala Ala Leu Asp Leu Ile Glu Arg Met Leu Thr Phe
419     290             295             300
422 Asn Pro Leu Gln Arg Ile Thr Val Glu Glu Ala Leu Glu His Pro Tyr
423 305             310             315             320
426 Leu Glu Arg Leu His Asp Val Ala Asp Glu Pro Ile Cys Thr Asp Pro
427             325             330             335
430 Phe Ser Phe Asp Phe Glu Gln His Pro Leu Thr Glu Asp Gln Met Lys
431             340             345             350
434 Leu Ile Pro Glu Asn Glu Ala Leu Glu Leu Asn Pro Asn Phe Arg Tyr
435         355             360             365
438 <210> SEQ ID NO: 10
439 <211> LENGTH: 371
440 <212> TYPE: PRT
441 <213> ORGANISM: Nicotiana tabacum
443 <400> SEQUENCE: 10
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**RAW SEQUENCE LISTING ERROR SUMMARY**    DATE: 06/21/2006
PATENT APPLICATION:    **US/10/768,886B**    TIME: 15:18:19

Input Set  : **A:\MAPK5 (Supp).txt**
Output Set: **N:\CRF4\06212006\J768886B.raw**

<u>Invalid <213> Response:</u>
Use of "Artificial" only as "<213> Organism" response is incomplete,
per 1.823(b) of New Sequence Rules. Valid response is Artificial Sequence.

Seq#:5,6,7,8

L:10 M:270 C: Current Application Number differs, Replaced Current Application Number